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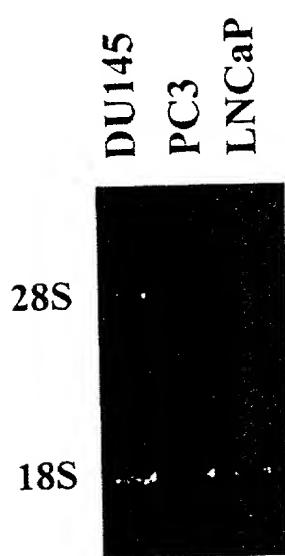


FIG.1A

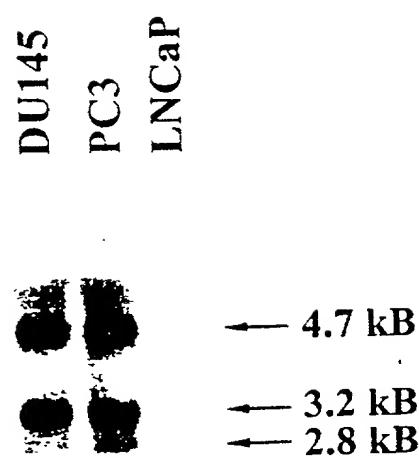


FIG.1B

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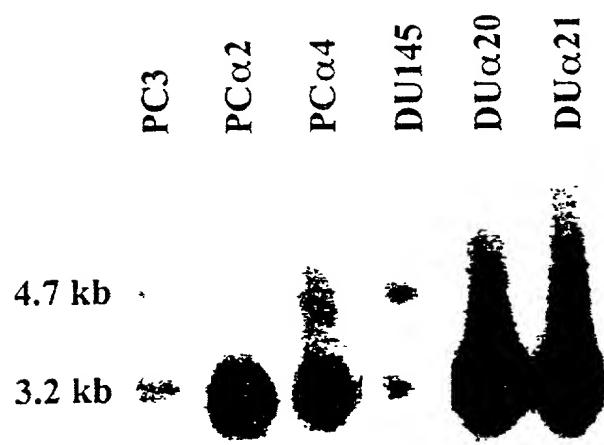


FIG. 2

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DU145

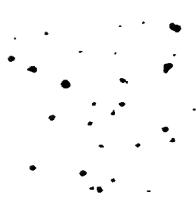
DU α 20DU α 21

FIG.3A



PC3

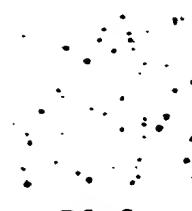
PC α 2PC α 4

FIG.3B

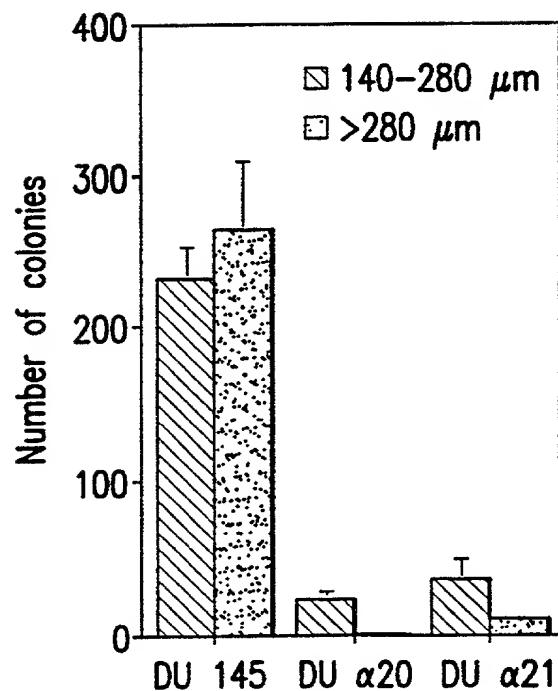


FIG.3A-1

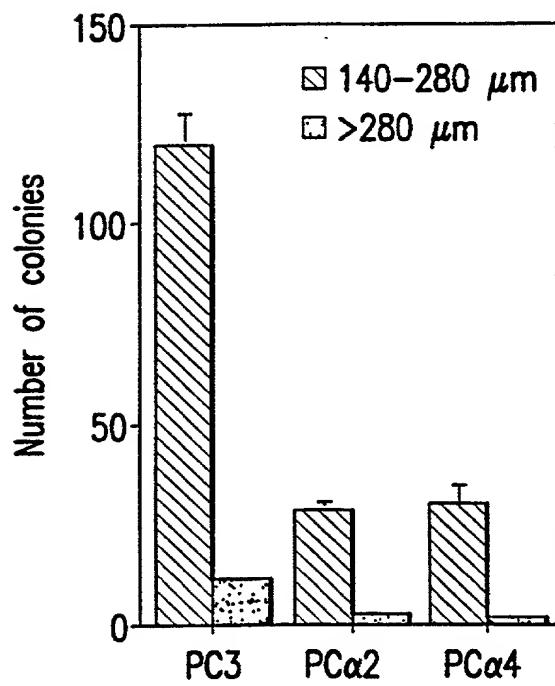


FIG.3B-1

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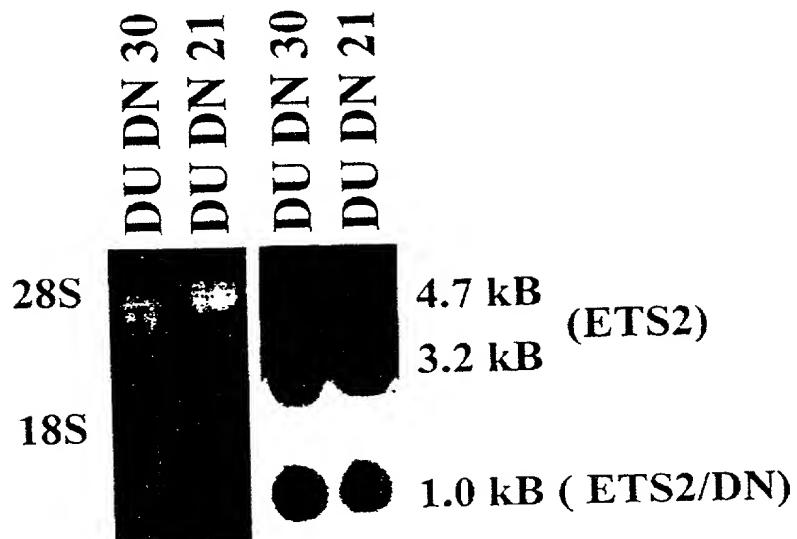


FIG.4A

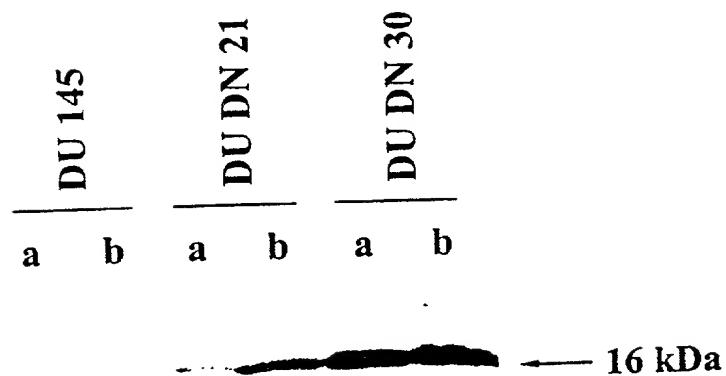


FIG.4B

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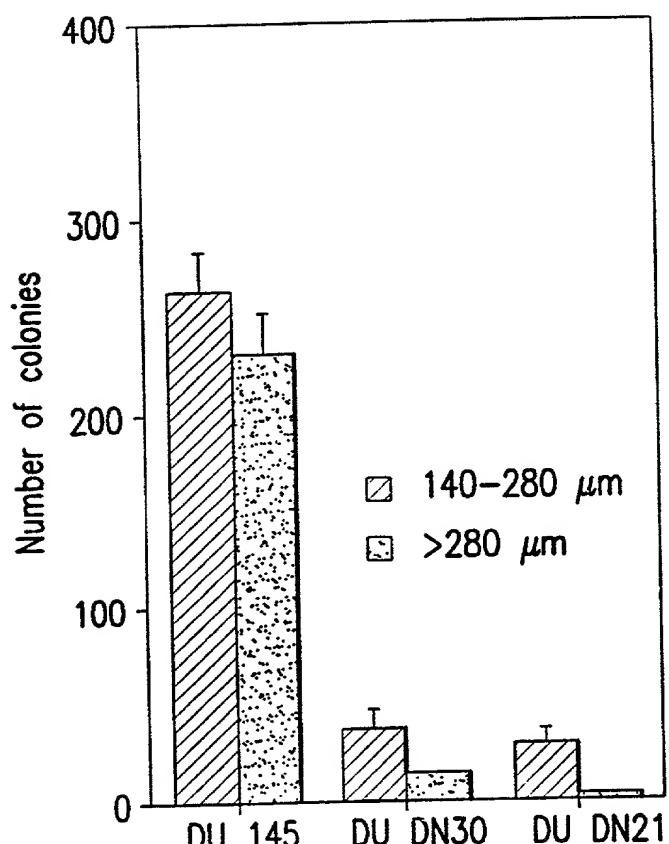


FIG.5

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CCGTTTCCTC	CCCTCCCCTC	CACTCGGCCG	TCCCTCCCTC	CTCCCTCCCTC	CTCCCTCCCTC	60
CTCCCCCTCC	TGAAGAGCCG	GCCCCGTGGC	GGACGGCCCC	GTTACTTCCT	CCAGAGACTG	120
ACGAGTGCAG	TGTCGCTCCA	GCTCAGAGCT	CCCGGAGCCG	CCCGGCCAGC	GTCCGGCCCTC	180
CCTGATCCTC	TCTGGCCGGC	GCCCTCGCCC	TCGCCCCGGC	CCGACCCGAGC	AGCCGCGGGC	240
CCCCACCAC	CACCGTCCCC	ACCAAGGCCG	GGCCCTGCC	GCAGCCGAGC	GATGAATGAT	300
TTCCGAATCA	AGAATATGGA	CCAGCTAGCC	CCTGTGGCTA	ACAGTTACAG	AGGGACACTC	360
AAGGCCACG	CAGCCTTGA	CACCTTGAT	GGGTCCCTGT	TTGCTGTTT	TCCTTCTCTA	420
AATGAAGACG	AAACACTCCA	AGAAGTCCCA	ACAGGCTTCG	ATTCCATTTC	TCATGACTCC	480
GCCAAGTGTG	AATTGCCCTT	GTAAACCCG	TGCAGCAAGG	CTGTGATGAG	TCAAGCCTTA	540
AAAGCTACCT	TCAGTGGCTT	CAAAAAGAA	CAGCGGCCGC	TCGGCATTCC	AAAGAACCCC	600
TGGCTGTGGA	GTGAGCAACA	GGTATGCCAG	TGGCTTCTCT	GGGCCACCAA	TGAGTTCACT	660
CTGGTGAACC	TCAATCTGCA	GAGGTTCCGC	ATGAATGGCC	AGATGCTGTG	TAACCTTGGC	720
AAGGAACGCT	TTCTGGAGCT	GGCACCTGAC	TTTGTGGCTG	ACATTCTCTG	CGAACATCTG	780
GAGCAAATGA	TCAAAGAAAA	CCAAGAAAAG	ACAGAAGATC	AATATGAAGA	AAATTACACAC	840
CTCACCTCCG	TTCCTCATTC	GATTAACAGC	AATACATTAG	GTTTGGCAC	AGAGCAGGGC	900
CCCTATGGAA	TCCAGACACA	GAATTACCCC	AAAGGCCGCC	TCCTGGACAG	CATGTCTCCG	960
CCCTCCACAC	CCAGCGTACT	CAGCTCTGAG	CAGGAGTTTC	AGATGTTCCC	CAAGTCTCGG	1020
CTCAGCTCCG	TCAGCGTCAC	CTACTGCTCT	GTCAGTCAGG	ACTTCCAGG	CAGCAACTTG	1080
AATTGCTCA	CCAACAATT	TGGGACTCCC	AAAGACCACG	ACTCCCCTGA	GAACGGTGGC	1140
GACAGCTTCG	AGAGCTCAGA	CTCCCTCCCTC	CAGTCCTGGA	ACAGCCAGTC	GTCCTTGGCTG	1200
GATGTGCAAC	GGGTTCCCTC	CTTCGAGAGC	TTCGAAGATG	ACTGCAGCCA	GTCTCTCTGC	1260
CTCAATAAGC	CAACCATGTC	TTCAAGGAT	TACATCCAAG	AGAGGAGTGA	CCCAGTGGAG	1320
CAAGGCAAAC	CAGTTATACC	TGCAGCTGTG	CTGGCCGGCT	TCACAGGAAG	TGGACCTATT	1380
CAGCTGTCCC	AGTTTCTCCT	GGAGCTGCTA	TCAGACAAAT	CCTGCCAGTC	ATTCATCAGC	1440
TGGACTGGAG	ACGGATGGG	GTTTAAGCTC	CCCCACCCCG	ATGAGGTGGC	CCGCCGGTGG	1500
GGAAAGAGGA	AAAATAAGCC	CAACATGAAC	TACGAGAAGC	TGAGCCGGGG	CTTACGCTAC	1560
TATTACGACA	AGAACATCAT	CCACAAGACG	TCGGGAAGC	GCTACGTGTA	CCGCTTCTGT	1620
TGCGACCTCC	AGAAACTTGCT	GGGGTTCACT	CCCGAGGAAC	TGCACGCCAT	CCTGGGCGTC	1680
CAGCCGACA	CGGAGGACTG	AGGTCCCGG	GACCACCTG	AGCCGGCCCC	AGGCTCGTGG	1740
ACTGAGTGGG	AAGCCCATCC	TGACCACTG	CCTCCGAGGA	CCCAGGAAAG	GCAGGATTGA	1800
AAATGTCCAG	GAAACTCCCC	AAACACCGAT	GGCCTTATTG	CATCCCCAAC	CACGCCCTTT	1860
GACCAGGCTG	CCTCCCTTGT	GGCAGCAACG	GCACAGCTAA	TTCTACTCAC	AGTGCTTTA	1920
AGTGAAAATG	GTCGAGAAAG	AGCCACCCGG	AAGCCGTCCCT	GGCCGCTGGC	AGTCCGTGGG	1980
ACGGGATGGT	TCTGGCTGTT	TGAGATTCTC	AAAGGAGCGA	GCATGTCGTG	GACACACACA	2040
GACTATTTT	AGATTTCTT	TTGCCCTTTG	CAACCAGGAA	CAGCAAATGC	AAAAACTCTT	2100
TGAGAGGGTA	GGAGGGTGGG	AAGGAACAA	CCATGTCATT	TCAGAAGTTA	GTTGTATAT	2160
ATTATAATAA	TCTTATAATT	GTTCAGAA	TCCCTTAACA	GTTCGTTATTA	ACAGAAATTG	2220
TATATTGTAA	TTAAAATAA	TTATATAACT	GTATTTGAAA	TAAGAATTG		2269

FIG.6

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Met Asn Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala
 1 5 10 15
 Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe
 20 25 30
 Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr
 35 40 45
 Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala
 50 55 60
 Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser
 65 70 75 80
 Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg
 85 90 95
 Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys
 100 105 110
 Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn
 115 120 125
 Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys
 130 135 140
 Glu Arg Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp
 145 150 155 160
 Glu His Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp
 165 170 175
 Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn
 180 185 190
 Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln
 195 200 205
 Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala
 210 215 220
 Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro
 225 230 235 240
 Lys Ser Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln
 245 250 255
 Asp Phe Pro Gly Ser Asn Leu Asn Leu Leu Thr Asn Asn Ser Gly Thr
 260 265 270
 Pro Lys Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser
 275 280 285
 Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp
 290 295 300
 Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln
 305 310 315 320
 Ser Leu Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln
 325 330 335

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Glu Arg Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala
340 345 350
Val Leu Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe
355 360 365
Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp
370 375 380
Thr Gly Asp Gly Trp Glu Phe Lys Lau Ala Asp Pro Asp Glu Val Ala
385 390 395 400
Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys
405 410 415
Leu Ser Arg Gly Leu Arg Tyr Tyr Asp Lys Asn Ile Ile His Lys
420 425 430
Thr Ser Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn
435 440 445
Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln
450 455 460
Pro Asp Thr Glu Asp
465

FIG.7B

ET51	HUMAN	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ET51	MOUSE	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETSB	CHICK	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETSA	XENLA	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
vETS	E26	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETS2	XENLA	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETS2	HUMAN	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETS2	MOUSE	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETS2	CHICK	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETS2	SEUR	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
ETS2	DROME	SG-P1QLWQFLLELLTDKS-COFS I SWTG-DGWEFKL S--DPDEVARRWGKRK-WEPKMNYEKL SRLRYYDKNI IRKTA-GKRYVYRFV-
FL11	MOUSE	SG-Q1QLWQFLLELLSDSA-NASCITWEG-TNGEFKMT--DPDEVARRWGERK-SKPMMNYDKL SRALRYYDKNIMTKVH-GKRYAYKFD-
ERG	HUMAN	SG-Q1QLWQFLLELLSDSS-NASCITWEG-TNGEFKMT--DPDEVARRWGERK-SKPMMNYDKL SRALRYYDKNIMTKVH-GKRYAYKFD-
ETS3	DROME	GSGCQIQ WQPLLELLSDSN-NASCITWEGTNG EFKLT--DPDEVARRWGERK-SKPMMNTDKL SRALR
ETS6	DROME	SGCGQIQ WQPLLELLADSS-NANAISWEG-QSGEFRLI--DPDEVARRWGERK-AKPMMNYDKL SRALRYYDKNIMTEVH-GKRYAYKFD-
GABP	RAT	NG-Q1QLWQFLLELLTDKD-ARDCISWVG-DEGEFKLN--QPELVAQKGQRK-NKPTMNYPKL SRALRYYDGDM1CKVQ-GKGFVYKFV-
DELG	DROME	NG-QVQLWQFLLEILTDCE-HDVIEWWG-TEGEFKLT--DPDRVARIWGEKK-NKPTMNYPKL SRALRYYDGDM1SKVS-SQKFVYKFV-
PEA3	MOUSE	RGA-LQLWQFLVALDDPT-NARFLAWTG-RQMEFKLI--EPEEVARLWIG1QK-NRPMAMNYDKL SRSLRYYEKG IMQKVA-GERYVYKFV-
ELK	HUMAN	MOPSVTLWQFLLQLREQG-NGCHIISNTSRDGCEFKLV--DAEEVARLWGLRK-NKTNMNTDKLSRALRYYQKNIIRKVS-GQKFVYKFV-
SAP1	HUMAN	MDSAITLWQFLLQLQKPO-NKMICWTSDG-QFKL--QAEEVARLWIG1RK-NKPMAMNYDKL SRALRYYVKNIIKVN-GQKVYKFVSL
ELKX	MOUSE	LWQFLLLLLLDQN-HDHLICNTSNDG-QFKL--KAEEVAKLWGLRK-NE TMNMYDKL SRALR
ELF1	HUMAN	KGNITYLWEIFLALLQDKATCPKYIKWTQREKGIFKLV--DSKAVSRLWGKHK-NKEDMNYE TMGRALRYYQORG ILAKVE-GQRVLIQFK
E74A	DROME	EGSTTYLWEFLKLQLQDREYQPRFIKWTREREKGIPKL V--DSKAVSRLWGMLHK-NKEDMNYE TMGRALRYYQORG ILAKVD-GQRVLVHFV
ETS4	DROME	GGSIIHLWQFLKELLASPVQNGTAIRWIDRSKGIPKIE--DSVRVAKLWGRRK-NRPAMNYDKL LRS1RQYYKKG IMKKSERSQRQLVYQFC
PUI	MOUSE	SKKK1IRLYQFLDDLLRSQDM-KDSIWWWDKDGTFQFSSKHKEALAHRWG1QKGCRNKKNTYQKMARALRNHYGTGEVKVKV--KKLTYQF-S
PUI	HUMAN	SKKK1IRLYQFLDDLLRSQDM-KDSIWWWDKDGTFQFSSKHKEALAHRWG1QKGCRNKKNTYQKMARALRNHYGTGEVKVKV--KKLTYQF-S

SUBSTITUTE SHEET (RULE 26)

FIG. 8A

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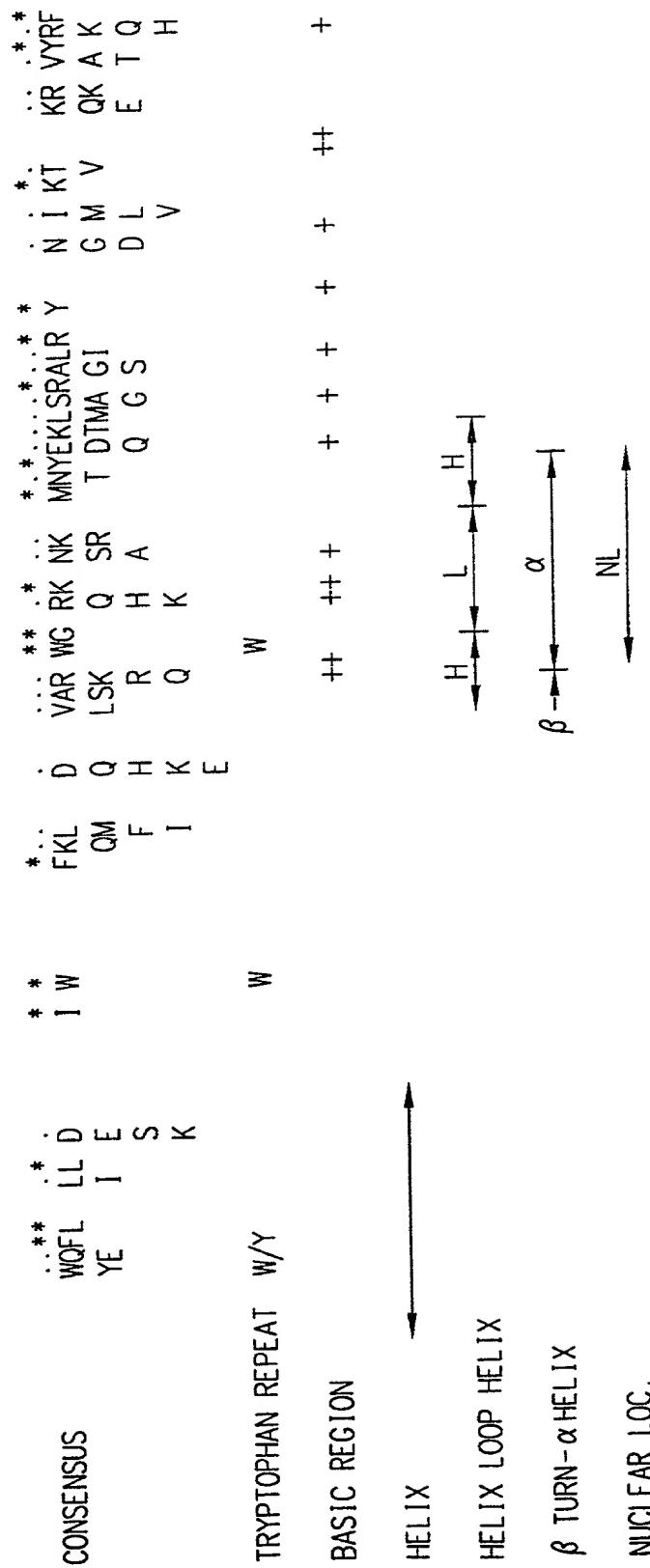


FIG.8B

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ETS2 IN 289

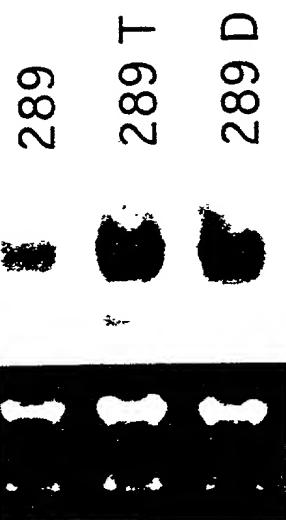


FIG.9A

ETS1 IN 289

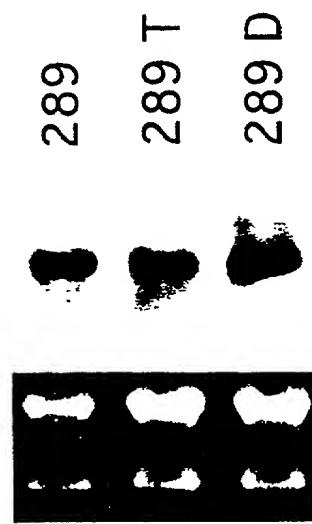


FIG.9B

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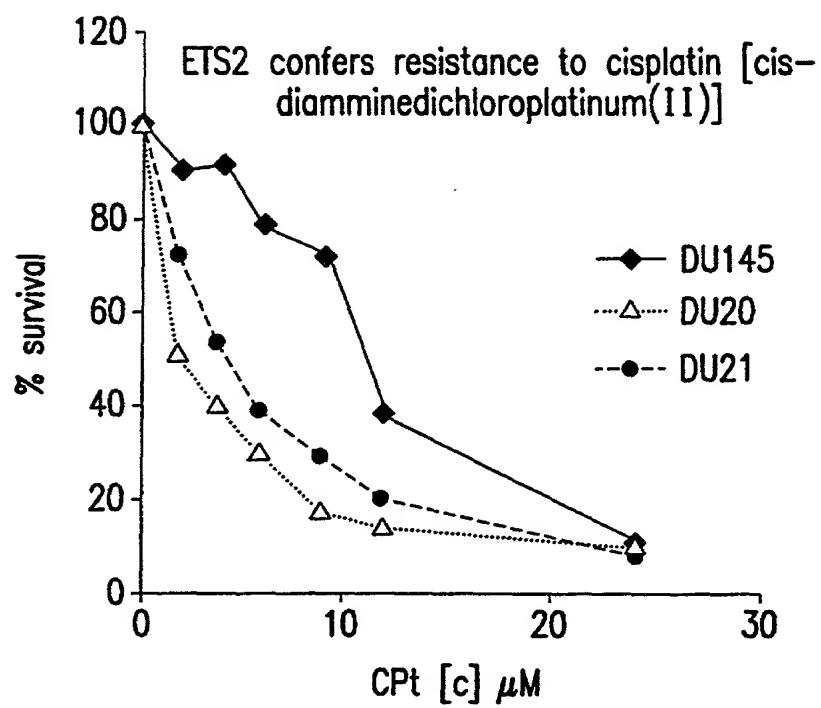


FIG.10